



FIG. 1

ATGGCGGATTCCAGCGAAGGCCCCGCGCGGGGCCCCGGGGAGGTGGCTGAGCTCCCCGGGGATG  
AGAGTGGCACCCAGGTGGGGAGGCTTTTCTCTCTCTCTCCCTGGCCAATCTGTTTGAGGGGGA  
GGATGGCTCCCTTTTCGCCCTCACCGGCTGATGCCAGTCGCCCTGCTGGCCAGGCGATGGGCGA  
CCAAATCTGCGCATGAAGTTCCAGGGCGCCTTCCGCAAGGGGGTGCCCAACCCCATCGATCTGC  
TGGAGTCCACCCTATATGAGTCCTCGGTGGTGCCTGGGCCCCAAGAAAGCACCCATGGACTCACT  
GTTTGACTACGGCACCTATCGTCACCACTCCAGTGACAACAAGAGGTGGAGGAAGAAGATCATA  
GAGAAGCAGCCGAGAGCCCCAAAGCTCCCGCCCCCTCAGCCGCCCCCATCCTCAAAGTCTTCA  
ACCGGCCCATCCTCTTTGACATCGTGTCCCGGGGCTCCACTGCTGACCTGGACGGGCTGCTCCC  
ATTCTTGCTGACCCACAAGAAACGCCTAACTGATGAGGAGTTTCGGGAACCATCTACGGGGAAG  
ACCTGCCTGCCCAAGGCCCTTGCTGAACCTGAGCAATGGCCGCAACGACACCATCCCTGTGCTGC  
TGGACATCGCGGAGCGCACCGGCAACATGAGGGAGTTCATTAACCTCGCCCTTCCGTGACATCTA  
CTATCGAGGGCAGACAGCCCTGCACATCGCCATTGAGCGTCGCTGCAAACACTACGTGGAACCTT  
CTCGTGGCCAGGGAGCTGATGTCCACGCCAGGCCCGTGGGCGCTTCTTCCAGCCCAAGGATG  
AGGGGGGCTACTTCTACTTTGGGGAGCTGCCCTGTGCTGGCTGCCTGCACCAACCAGCCCCA  
CATTGTCAACTACCTGACGGAGAACCCCCACAAGAAGGCGGACATGCGGCGCCAGGACTCGCGA  
GGCAACACAGTGCTGCATGCGCTGGTGGCCATTGCTGACAACACCCGTGAGAACACCAAGTTTG  
TTACCAAGATGTACGACCTGCTGCTGCTCAAGTGTGCCCGCCTCTTCCCCGACAGCAACCTGGA  
GGCCGTGCTCAACAACGACGGCCTCTCGCCCCCTCATGATGGCTGCCAAGACGGGCAAGATTGGG  
GTCTTTTACGACATCATCCGGCGGGAGGTGACGGATGAGGACACACGGCACCTGTCCCGCAAGT  
TCAAGGACTGGGCCTATGGGCCAGTGATTTCTCGCTTTATGACCTCTCTCTCCCTGGACACGTG  
TGGGGAAGAGGCCCTCCGTGCTGGAGATCCTGGTGTACAACAGCAAGATTGAGAACCGCCACGAG  
ATGCTGGCTGTGGAGCCCATCAATGAACTGCTGCGGGACAAGTGGCGCAAGTTCCGGGGCCGTCT  
CCTTCTACATCAACGTGGTCTCTTACCTGTGTGCCATGGTCATCTTCACTCTCACCGCCTACTA  
CCAGCCGCTGGAGGGCACACCGCCGTACCCTTACCGCACCCAGGTGGACTACCTGCGGCTGGCT  
GGCGAGGTCAATTACGCTCTTCACTGGGGTCTGTTCTTCTTACCAACATCAAAGACTTGTTCA  
TGAAGAAATGCCCTGGAGTGAATTCTCTCTTCAATTGATGGCTCCTTCCAGCTGCTCTACTTCAT  
CTACTCTGTCTGTTGATCGTCTCAGCAGCCCTCTACCTGGCAGGGATCGAGGCCTACCTGGCC  
GTGATGGTCTTTGCCCTGGTCTTGGGCTGGATGAATGCCCTTTACTTCAACCGTGGGCTGAAGC  
TGACGGGGACCTATAGCATCATGATCCAGAAGATTCTCTTCAAGGACCTTTTCCGATTCTGCT  
CGTCTACTTGCTCTTTCATGATCGGCTACGCCTCAGCCCTGGTCTCCCTCCTGAACCCGTGTGCC  
AACATGAAGGTGTGCAATGAGGACCAGACCAACTGCACAGTGCCCACTTACCCCTCGTGCCGTG  
ACAGCGAGACCTTCAGCACCTTCCTCCTGGACCTGTTTTAAGCTGACCATCGGCATGGGCGACCT  
GAGATGCTGAGCAGCACCAAGTACCCCGTGGTCTTCATCATCCTGCTGGTGACCTACATCATCC  
TCACCTTTGTGCTGCTCCTCAACATGCTCATTGCCCTCATGGGCGAGACAGTGGGCCAGGTCTC  
CAAGGAGAGCAAGCACATCTGGAAGCTGCAGTGGGCCACCACCATCCTGGACATTGAGCGCTCC  
TTCCCCGTATTCTGAGGAAGGCCCTTCCGCTCTGGGGAGATGGTCACCGTGGGCAAGAGCTCGG  
ACGGCACTCCTGACCGCAGGTGGTGGTTCAGGGTGAATGAGGTGAACTGGTCTCACTGGAACCA  
GAACTTGGGCATCATCAACGAGGACCCGGGCAAGAATGAGACCTACCAGTATTATGGCTTCTCG  
CATAACCGTGGGCCGCTCCGCGAGGGATCGTGGTCTCGGTGGTACCCCGCGTGGTGGAACCTGA  
ACAAGAACTCGAACCCGGACGAGGTGGTGGTGCCTCTGGACAGCATGGGGAACCCCCGCTGCGA  
TGGCCACCAGCAGGGTTACCCCGCAAGTGGAGGACTGATGACGCCCGCTCTAGGGACTGCAG  
CCCAGCCCCAGCTTCTCTGCCCACTCATTTCTAGTCCAGCCGATTTTACGAGTGCCCTTCTGGG  
GTGTCCCCCACACCCTGCTTTGGCCCCAGAGGCGAGGGACAGTGGAGGTGCCAGGGAGGCCC  
CAGGACCCTGTGGTCCCTGGCTCTGCCTCCCCACCCTGGGGTGGGGGCTCCCGGCCACCTGTC  
TTGCTCCTATGGAGTCACATAAGCCA



## FIG. 2

MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGED  
GSLSPSPADASRPAGPGDGRPNLRMKFQGAFRKGVNPIDLLESTLYESSVVPGPKKA  
PMDSLFDYGTyrHHSSDNKRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSR  
GSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAE  
RTGNMREFINSFPRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPK  
DEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADN  
TRENTKFVTKMYDLLLLLKCARLEFPDSNLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRR  
EVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVYNSKIENRHEML  
AVEPINELLRDKWRKFGAVSFYINVVSYLCAVIFTLTAYYQPLEGTPPYPYRTTVDY  
LRLAGEVITLFTGVLFFFTNIKDLEFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAAL  
YLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLF  
MIGYASALVSLNPNCANMKVCNEDQTNCTVPTYPSCRDSETFSTFLDLFKLTIGMGD  
LEMLSSTKYPVVFIIILLVTYIILTFVLLLNMLIALMGETVGQVSKEKHIWKLQWATT  
ILDIERSFVFLRKAFRSGEMVTVGKSSDGTDDRWCFRVNEVNWSHWNQNLGIINED  
PGKNETYQYYGFSHTVGRLRRDRWSSVVPVVELNKN SNPDEVVPLDSMGNPRCDGH  
QQGYPRKWRTDDAPL

FIG. 3

AGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCC  
AACGCGTTGGAGCTCTCCCATATGGTCGACCTGCAGCGGCCGCGAATTCAGTAGTGATTATGGC  
GGATTCAGCGAAGGCCCCCGCGCGGGGGCCCGGGGAGGTGGCTGAGCTCCCCGGGGATGAGAGT  
GGCACCCAGGTGGGGAGGCTTTTCTCTCTCTCTCCCTGGCCAATCTGTTTGAGGGGGAGGATG  
GCTCCCTTTTCGCCCTCACCGGCTGATGCCAGTCGCCCTGCTGGCCCAGGCGATGGGCGACCAA  
TCTGCGCATGAAGTTCAGGGCGCCTTCGCGAAGGGGGTGCCCAACCCCATCGATCTGCTGGAG  
TCCACCCTATATGAGTCCTCGGTGGTGCCTGGGCCCCAAGAAAGCACCCATGGACTCACTGTTTG  
ACTACGGCACCTATCGTCAACCACTCCAGTGACAACAAGAGGTGGAGGAAGAAGATCATAGAGAA  
GCAGCCGAGAGCCCCAAAGCCCCCTGCCCTCAGCCGCCCCCATCCTCAAAGTCTTCAACCGG  
CCTATCCTCTTTGACATCGTGTCCCGGGGCTCCACTGCTGACCTGGACGGGCTGCTCCCATTTCT  
TGCTGACCCACAAGAAACGCCTAACTGATGAGGAGTTTCGAGAGCCATCTACGGGGAAGACCTG  
CCTGCCCAAGGCCTTGCTGAACCTGAGCAATGGCCGCAACGACACCATCCCTGTGCTGCTGGAC  
ATCGCGGAGCGCACCGGCAACATGCGGGAGTTCATTAACCTCGCCCTTCCGTGACATCTACTATC  
GAGGTCAGACAGCCCTGCACATCGTCATTGAGCGTCGCTGCAAACACTACGTGGAACCTTCTCGT  
GGCCCAGGGAGCTGATGTCCAGCCCCAGGCCCGTGGGCGCTTCTTCCAGCCCAAGGATGAGGGG  
GGCTACTTCTACTTTGGGGAGCTGCCCCGTGTCGCTGGCTGCCTGCACCAACCAGCCCCACATTG  
TCAACTACCTGACGGAGAACCCCCACAAGAAGGCGGACATGCGGCGCCAGGACTCGCGAGGCAA  
CACAGTGCTGCATGCGCTGGTGGCCATTGCTGACAACACCCGTGAGAACACCAAGTTTGTACC  
AAGATGTACGACCTGCTGCTGCTCAAGTGTGCCCGCCTCTTCCCCGACAGCAACCTGGAGGCCG  
TGCTCAACAACGACGGCCTCTCGCCCCCTCATGATGGCTGCCAAGACGGGCAAGATTGGGATCTT  
TCAGCACATCATCCGGCGGGAGGTGACGGATGAGGACACACGGCACCTGTCCCGCAAGTTCAAG  
GACTGGGCCTATGGGCCAGTGATTCTCGCTTTATGACCTCTCCTCCCTGGACACGTGTGGGG  
AAGAGGCCTCCGTGCTGGAGATCCTGGTGTACAACAGCAAGATTGAGAACCGCCACGAGATGCT  
GGCTGTGGAGCCCATCAATGAACTGCTGCGGGACAAGTGGCGCAAGTTCGGGGCCGTCTCCTTC  
TACATCAACGTGGTCTCCTACCTGTGTGCCATGGTCATCTTCACTCTCACCGCCTACTACCAGC  
CGCTGGAGGGCACACCGCCGTACCCCTACCGCACACGGTGGACTACCTGCGGCTGGCTGGCGA  
GGTCATTACGCTCTTCACTGGGGTCTGTCTTCTTCAACCAACATCAAAGACTTGTTCATGAAG  
AAATGCCCTGGAGTGAATTCTCTCTTCAATTGATGGCTCCTTCCAGCTGCTCTACTTCATCTACT  
CTGTCTTGGTGATCGTCTCAGCAGCCCTCTACCTGGCAGGGATCGAGGCCTACCTGGCCGTGAT  
GGTCTTTGCCCTGGTCTTGGGCTGGATGAATGCCCTTTACTTCACCCGTGGGCTGAAGCTGACG  
GGGACCTATAGCATCATGATCCAGAAGATTCTCTTCAAGGACCTTTTCCGATTCTGTCTCGTCT  
ACTTGCTCTTCATGATCGGCTACGCTTCAGCCCTGGTCTCCCTCCTGAACCCGTGTGCCAACAT  
GAAGGTGTGCAATGAGGACCAGACCAACTGCACAGTGCCCACTTACCCCTCGTGCCGTGACAGC  
GAGACCTTCAGCACCTTCTCCTGGACCTGTTTAAAGCTGACCATTGGCATGGGCGACCTGGAGA  
TGCTGAGCAGCACCAAGTACCCCGTGGTCTTCATCATCCTGCTGGTGACCTACATCATCCTCAC  
CTTTGTGCTGCTCCTCAACATGCTCATTGCCCTCATGGGCGAGACAGTGGGCCAGGTCTCCAAG  
GAGAGCAAGCACATCTGGAAGCTGCAGTGGGCCACCACCATCCTGGACATTGAGCGCTCCTTCC  
CCGTATTCTTGAGGAAGGCCTTCCGCTCTGGGGAGATGGTCAACCGTGGGCAAGAGCTCGGACGG  
CACTCCTGACCGCAGGTGGTGCCTTCAGGGTGGATGAGGTGAACTGGTCTCACTGGAACCAGAAC  
TTGGGCATCATCAACGAGGACCCGGGCAAGAATGAGACCTACCAGTATTATGGCTTCTCGCATA  
CCGTGGGCGCCCTCCGCAGGGATCGCTGGTCTCGGTGGTACCCCGCGTGGTGGAACTGAACAA  
GAACTCGAACCCGGACGAGGTGGTGGTGCCTCTGGACAGCATGGGGAACCCCGCTGCGATGGC  
CACCAGCAGGGTTACCCCGCAAGTGGAGGACTGATGACGCCCCGCTCTAGGGACTGCAGCCCA  
GCCCCAGCTTCTCTGCCCCTCACTTCTAGTCCAGCCGCATTTACGAGTGCCCTTCTGGGGTGT  
CCCCCACACCCTGCTTTGGCCCCAGAGGCGAGGGACCAGTGGAGGTGCCAGGGAGGGCCCCAGG  
ACCCTGTGGTCCCCTGGCTCTGCCTCCCCACCCTGGGGTGGGGGCTCCCGGCCACCTGTCTTGC  
TCCTATGGAATCACTAGTGAATTCCCGCGGCCGCCATGGCGGCCGGGAGCATGCGACGTGGGGC  
CCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTGTTTTACAACGTGCTGACTG  
GGAAAACCTGCGTTACCCAACCTAATCGCCTTGACGACATCC



## FIG. 4

MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANL  
FEGEDGSLSPSPADASRPAGPGDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPGPKKAP  
MDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLD  
GLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPF  
RDIYYRGQTALHIVIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACT  
NQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPD  
SNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSS  
LDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTL  
TAYYQPLEGTPPYPPYRTTVDYLRRLAGEVITLFTGVLFFFTNIKDLEFMKKCPGVNSLFIDGSFQL  
LYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLF  
RFLLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTYPSCRDSETFSTFLDLFKLTIG  
MGDLEMLSSTKYPVVFIIILLVTYIIILTFVLLLNMLIALMGETVGQVSKEKHIWKLQWATTILD  
IERSFPVFLRKAFRSGEMVTVGKSSDGTDDRWCFRVDEVNWSHWNQNLGIINEDPGKNETYQY  
YGFSTVGRRLRRDRWSSVPRVVELNKNNSNPDEVVPLDSMGNPRCDGHQQGYPRKWRTDDAPL

**FIG. 5A**

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

## Secondary structure

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

## Secondary structure

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

## Secondary structure

	1	10	20	30	40	50
1	PGD	PRA	AGD	VAE	PPG	DEE
2	PGD	PRA	AGD	VAE	PPG	DEE
3	PGD	PRA	AGD	VAE	PPG	DEE
4	PGD	PRA	AGD	VAE	PPG	DEE
5	PGD	PRA	AGD	VAE	PPG	DEE
6	PGD	PRA	AGD	VAE	PPG	DEE
7	PGD	PRA	AGD	VAE	PPG	DEE
8	PGD	PRA	AGD	VAE	PPG	DEE
9	PGD	PRA	AGD	VAE	PPG	DEE
10	PGD	PRA	AGD	VAE	PPG	DEE
11	PGD	PRA	AGD	VAE	PPG	DEE
12	PGD	PRA	AGD	VAE	PPG	DEE
13	PGD	PRA	AGD	VAE	PPG	DEE
14	PGD	PRA	AGD	VAE	PPG	DEE
15	PGD	PRA	AGD	VAE	PPG	DEE
16	PGD	PRA	AGD	VAE	PPG	DEE
17	PGD	PRA	AGD	VAE	PPG	DEE
18	PGD	PRA	AGD	VAE	PPG	DEE
19	PGD	PRA	AGD	VAE	PPG	DEE
20	PGD	PRA	AGD	VAE	PPG	DEE
21	PGD	PRA	AGD	VAE	PPG	DEE
22	PGD	PRA	AGD	VAE	PPG	DEE
23	PGD	PRA	AGD	VAE	PPG	DEE
24	PGD	PRA	AGD	VAE	PPG	DEE
25	PGD	PRA	AGD	VAE	PPG	DEE
26	PGD	PRA	AGD	VAE	PPG	DEE
27	PGD	PRA	AGD	VAE	PPG	DEE
28	PGD	PRA	AGD	VAE	PPG	DEE
29	PGD	PRA	AGD	VAE	PPG	DEE
30	PGD	PRA	AGD	VAE	PPG	DEE
31	PGD	PRA	AGD	VAE	PPG	DEE
32	PGD	PRA	AGD	VAE	PPG	DEE
33	PGD	PRA	AGD	VAE	PPG	DEE
34	PGD	PRA	AGD	VAE	PPG	DEE
35	PGD	PRA	AGD	VAE	PPG	DEE
36	PGD	PRA	AGD	VAE	PPG	DEE
37	PGD	PRA	AGD	VAE	PPG	DEE
38	PGD	PRA	AGD	VAE	PPG	DEE
39	PGD	PRA	AGD	VAE	PPG	DEE
40	PGD	PRA	AGD	VAE	PPG	DEE
41	PGD	PRA	AGD	VAE	PPG	DEE
42	PGD	PRA	AGD	VAE	PPG	DEE
43	PGD	PRA	AGD	VAE	PPG	DEE
44	PGD	PRA	AGD	VAE	PPG	DEE
45	PGD	PRA	AGD	VAE	PPG	DEE
46	PGD	PRA	AGD	VAE	PPG	DEE
47	PGD	PRA	AGD	VAE	PPG	DEE
48	PGD	PRA	AGD	VAE	PPG	DEE
49	PGD	PRA	AGD	VAE	PPG	DEE
50	PGD	PRA	AGD	VAE	PPG	DEE

	60	70	80	90	100
PVD	ASRRPAGP	NLRMKFQG	NLRMKFQG	DLLESTL	YES
PRWT	ASRRPAGP	NLRMKf	NLRMKFQG	DLLESTL	YES
PAD	ASRRPAGP	NLRMKFQG	NLRMKFQG	DLLESTL	YES
PSDR	ASRRPAGP	NLRMKFQG	NLRMKFQG	DLLESTL	YES

KAPMDS	FDY	GT	YR	H	HP	SD	NK	RR	RR	KV	EK	Q	Q	SP	KA	PA	Q	Q	PP	PP	LK	VFN	
KAPMDS	FDY	GT	YR	H	HP	SD	NK	RR	RR	KV	EK	Q	Q	SP	KA	PA	Q	Q	PP	PP	LK	VFN	
KAPMDS	FDY	GT	YR	H	HP	SD	NK	RR	RR	KI	EK	Q	Q	SP	KA	PA	Q	Q	PP	PP	LK	VFN	
KAPMDS	FDY	GT	YR	C	HP	SE	NK	RR	RR	RV	EK	P	V	AG	T	KG	PA	P	N	PP	PP	V	LK

5  
6

FIG. 5B

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

Secondary structure

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

Secondary structure

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

Secondary structure

160 170 180 190 200  
RPI LFDI VSRGSTADL DGLLS YLL THKKRLTDEEFREPSTGKTCLPKALL  
RPI LFDI VSRGSTADL DGLLS YLL THKKRLTDEEFREPSTGKTCLPKALL  
RPI LFDI VSRGSTADL DGLLS YLL THKKRLTDEEFREPSTGKTCLPKALL  
RPI LFDI VSRGSTADL DGLLS YLL THKKRLTDEEFREPSTGKTCLPKALL  
RRSTFDAVAQSNCCQELLESLLPFLQRWSKKRLTDSAEFKDPETGKTCLPKALL  
RDRLFSVMVRGVPEELTGLLE YLLRWNSSKYLLTDSAEFKDPETGKTCLPKALL  
PLGKWEDHKACWQMQRGALGESLHVLN  
R I FshVupussittLpuLLsaLhccKcLT DptaccsutGKTCL KAIL

210 220 230 240 250  
NLSNGRNDTI PV LLDI AERTGNMREFINSPPFRDI YYRGQTALHI AERRC  
NLSNGRNDTI PV LLDI AERTGNMREFINSPPFRDI YYRGQTALHI AERRC  
NLSNGRNDTI PV LLDI AERTGNMREFINSPPFRDI YYRGQTALHI AERRC  
NLSAGRNDTI PI LLDI AEKTGNMREFINSPPFRDI YYRGQTALHI AERRC  
NLSHNGQNDTI AL LLDVARKTDSLKQFVNASTDESEYKQGQTALHI AERRC  
NLQDGVNACI MP LLDI DKDSGNPKPLVNACQCTDESEYKQGQTALHI AERRC  
REQQVCYEI ARV LLDI LKRV-----FPGMANDLYLGDEEQFGQSALHLAI VHDD  
CDSKVHTKLARV LLDI LKRV-----FPNLALDVMIEGE EYLGQSALHLAI VHSN  
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AR

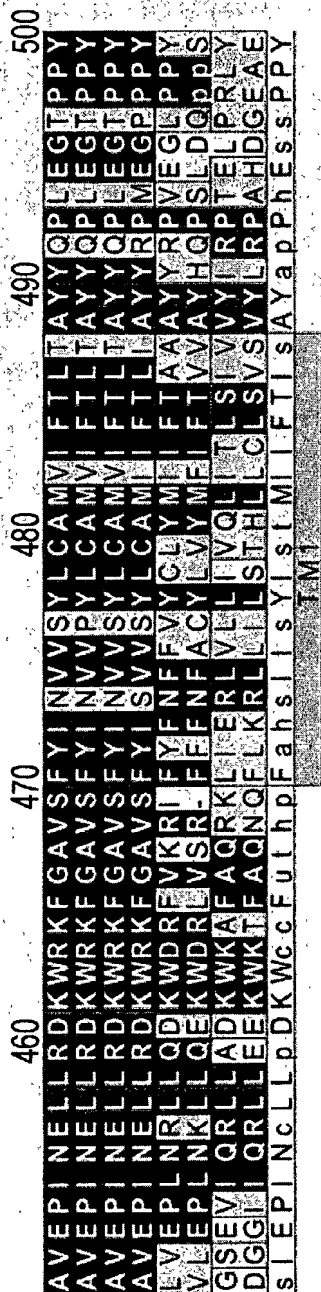
260 270 280 290 300  
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KHYVELLVEIKGADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHI  
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LQCVKLLVNGADVHLRAACGGRFFQKH-QGTCTFYFGEPLSLAACTKQWDV  
YETVSLLENSKADVNARACGGRFFLPEDEKLT nvyYGEYPLAAACFGNKDI  
NELVADLIEAGADIHQRAIGSFFFLPRDQQRANvMGEYPLAAACGANE SV  
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D1 ADR2

[illegible][illegible]

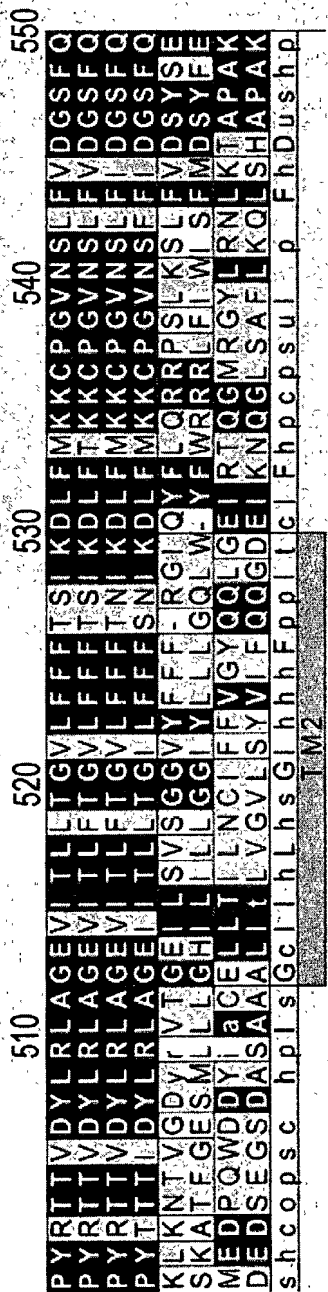
HL	SR	KF	KD	WA	Y	GP	V	SS	LY	DL	SS	LD	TC	GE	EV	SV	LE	LV	YN	SK	EN	RR	HE	ML	410	420	430	440	450																			
HL	SR	KF	KD	WA	Y	GP	V	SS	LY	DL	SS	LD	TC	GE	EV	SV	LE	LV	YN	SK	EN	RR	HE	ML																								
HL	SR	KF	KD	WA	Y	GP	V	SS	LY	DL	SS	LD	TC	GE	EV	SV	LE	LV	YN	SK	EN	RR	HE	ML																								
HL	SR	KF	KD	WA	Y	GP	V	SS	LY	DL	SS	LD	TC	GE	EV	SV	LE	LV	YN	SK	EN	RR	HE	ML																								
HL	SR	KF	TE	WA	Y	GP	VH	SS	LY	DL	SS	LD	TC	GE	EV	SV	LE	LV	YN	SK	EN	RR	HE	ML																								
PL	SR	KF	TE	WA	Y	GP	VH	SS	LY	DL	SS	LD	TC	GE	EV	SV	LE	LV	YN	SK	EN	RR	HE	ML																								
PL	SR	KF	TE	WA	Y	GP	VH	SS	LY	DL	SS	LD	TC	GE	EV	SV	LE	LV	YN	SK	EN	RR	HE	ML																								
PE	FW	RF	SD	MT	CS	AY	PL	NT	LD	TL	QP	DG	ST	NY	DS	-	WE	KN	SV	LE	IA	EH	CK	SS	PN	RR	HR	MM	V																			
RE	FW	RY	SN	IT	CS	GY	PL	NAL	DT	LL	P	D	GR	TN	WN	SA	FI	LN	GT	K	P	EH	LD	-	M	ML																						
c	L	S	R	K	F	p	c	w	s	Y	G	P	V	h	s	S	L	Y	D	L	S	s	I	D	o	s	s	c	p	s	S	I	L	I	I	s	SK	EN	RR	H	c	M	L					

## Secondary structure

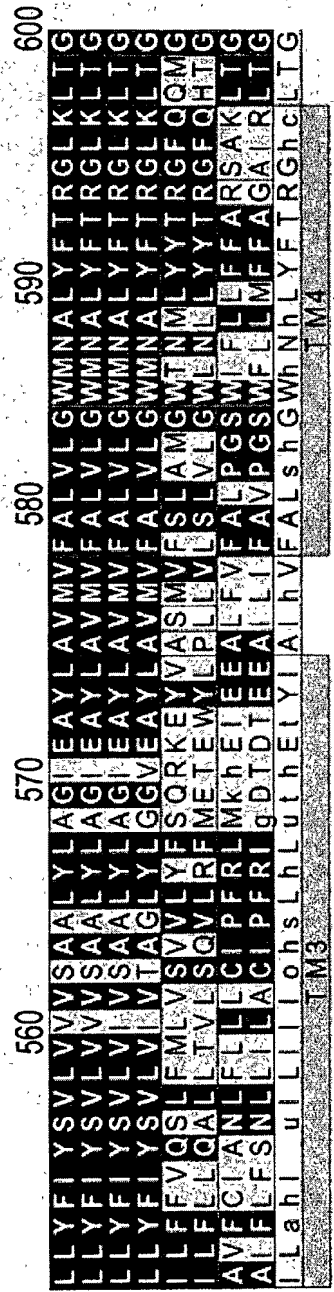
RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions



## Secondary structure



## Secondary structure



## Secondary structure



# FIG. 5E

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

610 620 630 640 650  
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVT LNPCTNMMKV CNEDQSS  
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVT LNPCTNMMKV CNEDQSS  
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVT LNPCTNMMKV CNEDQSS  
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVT LNPCTNMMKV CNEDQSS  
IYAVMI EKMI LRDLCRFMFVYLVFLFGFSAVALVT LIDGKNNSLPMESTP  
IYAVMI EKMI LRDLCRFMFVYLVFLFGFSAVALVT LIDGKNNSLPMESTP  
PFVQMI YSMI AGDMIRFAI ISAI FLVSFSQVFFYFGKMDMAKQKLEDTNP  
PFVQMI YSMI AGDMIRFAI ISAI FLVSFSQVFFYFGKMDMAKQKLEDTNP  
sYul MI pKhi hcdLhRfni VYLI FhGausAIVoLhpsst s phspcsp s

Secondary structure

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

660 670 680 690 700  
NCTVPSYPACRDSSEETFSAFLLDLDFKLTIGMGDLMLSSAKYPVVFILLLV  
NCTVPSYPACRDSSEETFSAFLLDLDFKLTIGMGDLMLSSAKYPVVFILLLV  
NCTVPSYPACRDSSEETFSAFLLDLDFKLTIGMGDLMLSSAKYPVVFILLLV  
NCTVPSYPACRDSSEETFSAFLLDLDFKLTIGMGDLMLSSAKYPVVFILLLV  
HKCRGSACKgNSYNSLYSTCLELDFKLTIGMGDLMLSSAKYPVVFILLLV  
TIVTEQPTVIGQepYRSLLDASLELDFKLTIGMGDLMLSSAKYPVVFILLLV  
HACRISGYTIIYTYNTFPETFI TLFRA SMGGYDYEEFSCANYQALTKTLFV  
---HPQVQSTMENTYTSTWMALFQITLGDYNYPLDNOTYPNLSKTVEF  
pssh ohssps pTasshhLcLFKhTIGMGDL Ehhpscy sVhIILLV

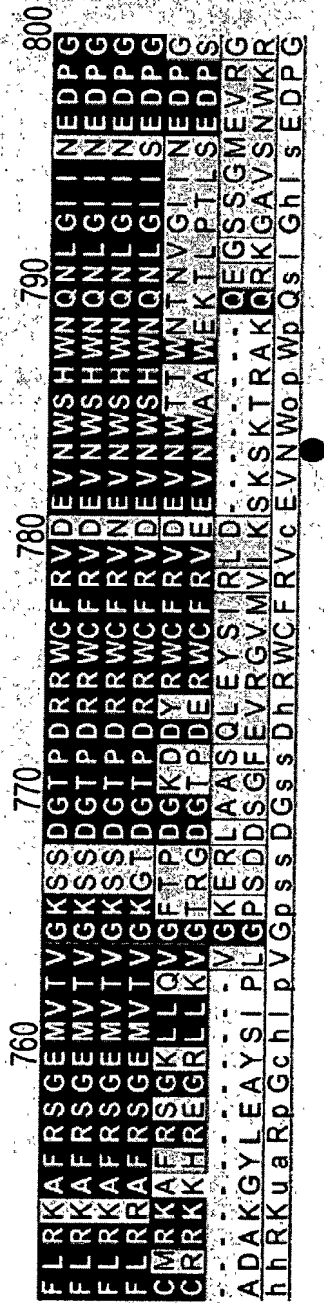
Secondary structure

RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions

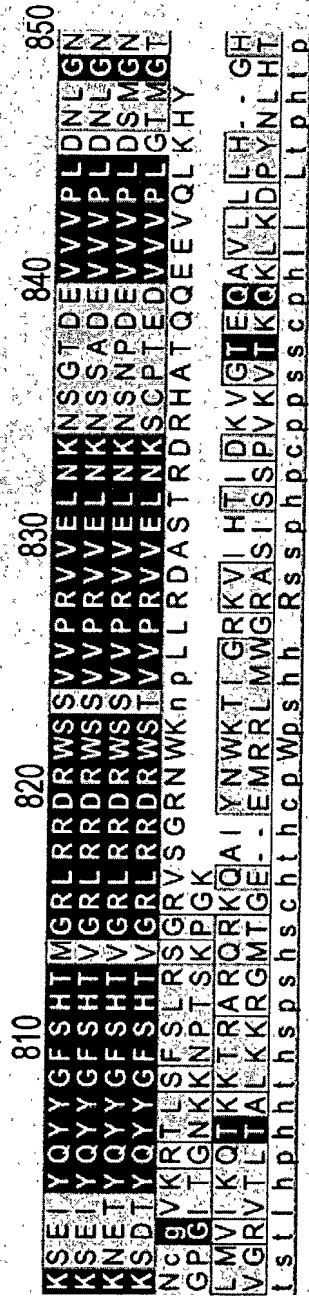
710 720 730 740 750  
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSSFPV  
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSSFPV  
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSSFPV  
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSSFPV  
AYVLLTYVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSSFPV  
AYVLLTYVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSSFPV  
LYMFVMPIMMNIAMMGNTYTIVIAQA EKAWRQQYAQI VMVLENGYWW  
IFMFEVPI LLLNMLIAMMGNTYTIVIAQA EKAWRQQYAQI VMVLENGYWW  
sYIILTLT a LLLNMLIALMGETVspVucpScclWKLQaApoilcIERSa h

Secondary structure

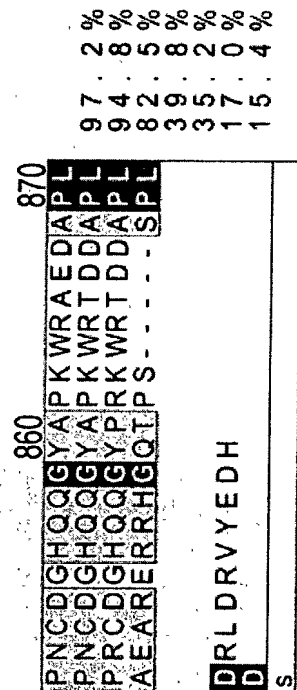
RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions



RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions



RnVR-MAC  
MmVR-MAC  
HsVR-MAC  
GgVR-MAC  
RnVR1  
RnVRL-1  
CeOSM-9  
DmCG4536  
Consensus  
Regions



## Secondary structure

AGENT & TRADEMARK OFF

FIG. 6A

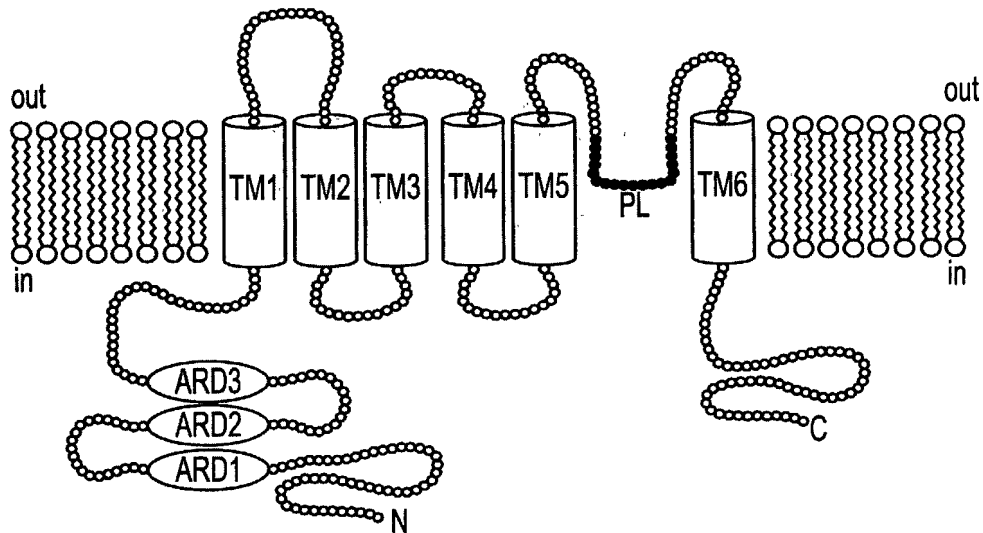


FIG. 6B

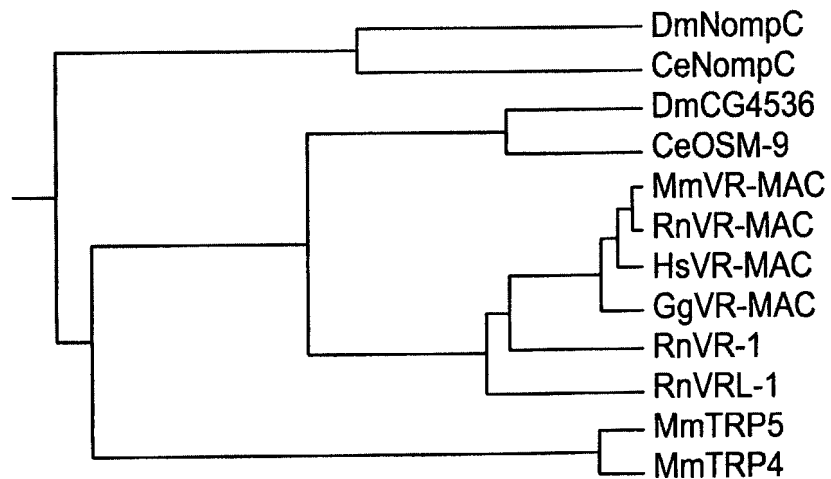




FIG. 7A

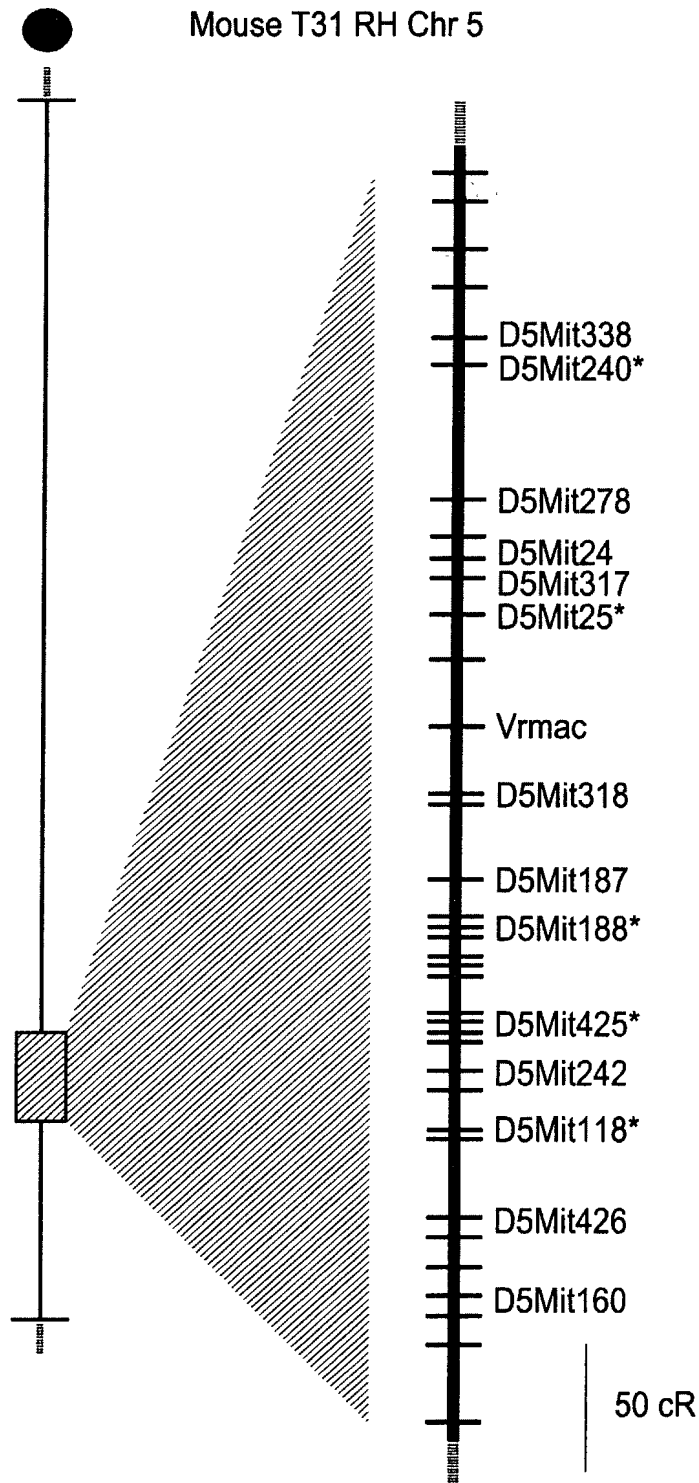




FIG. 7B

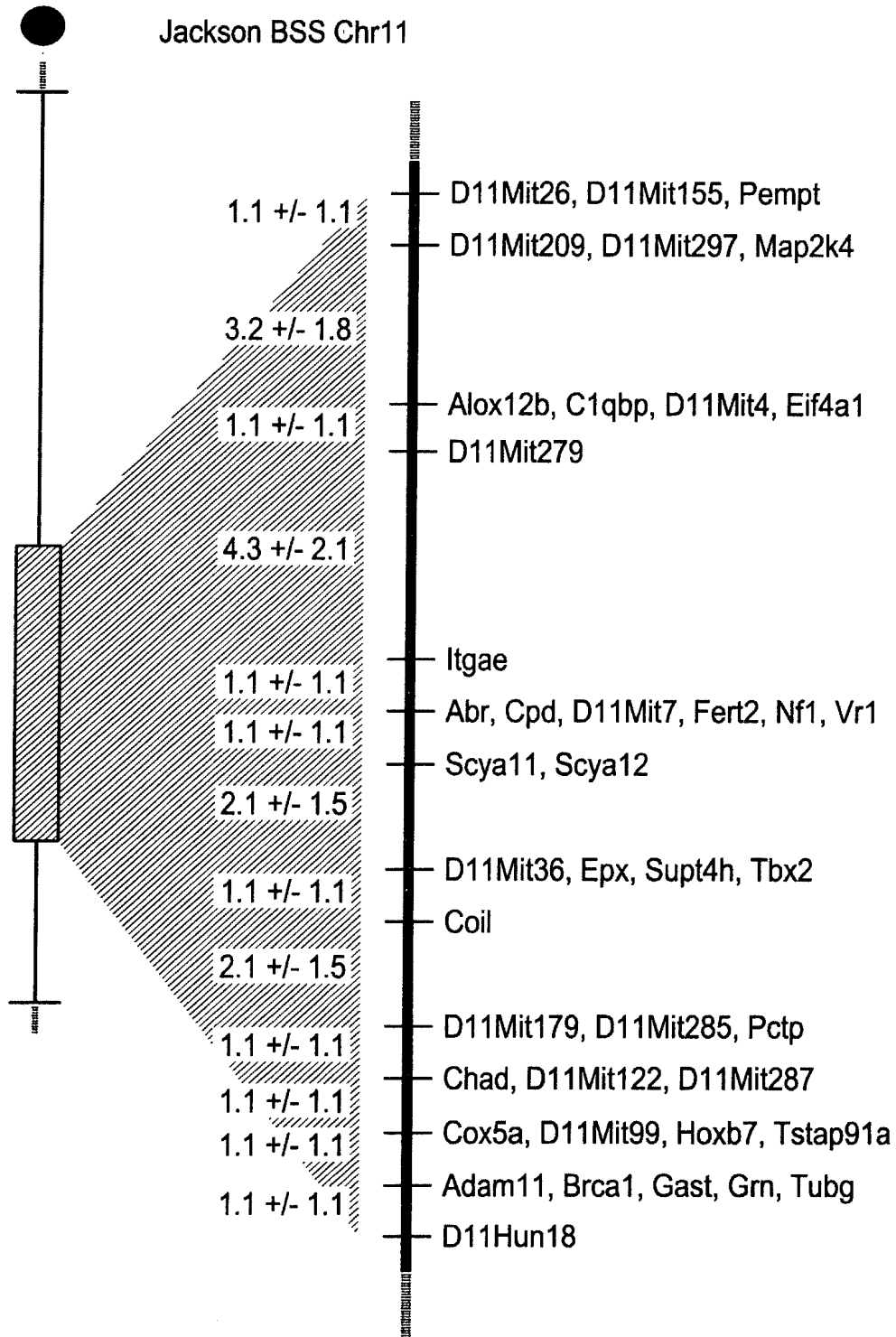
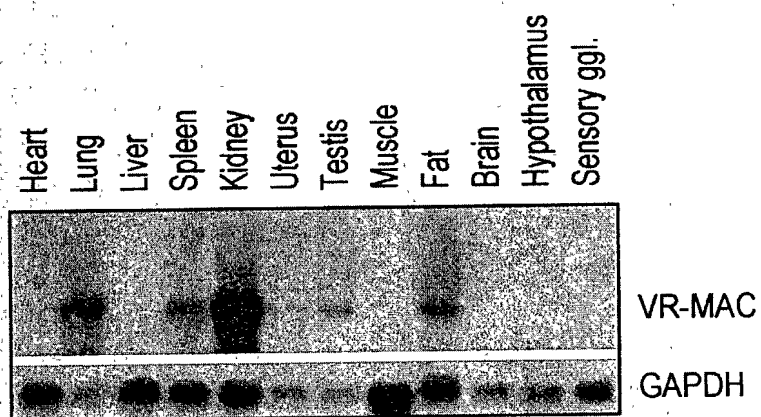


FIG. 8



PATENT & TRADE-MARK

FIG. 9A

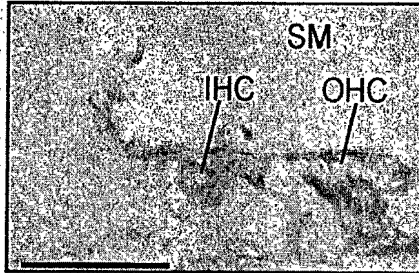


FIG. 9B

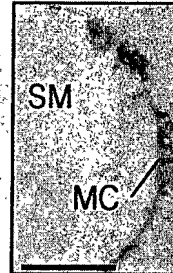


FIG. 9E

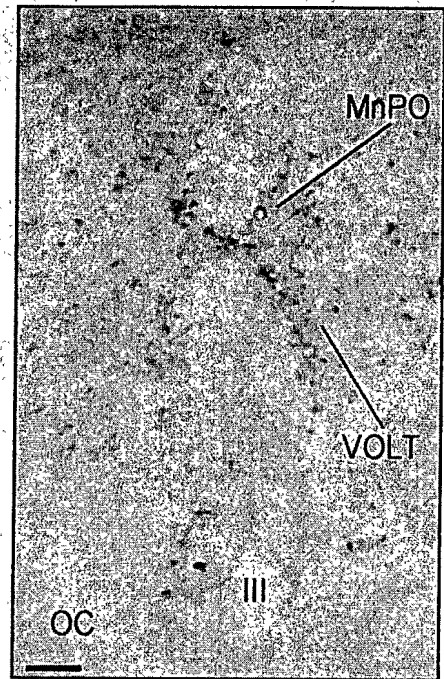


FIG. 9C

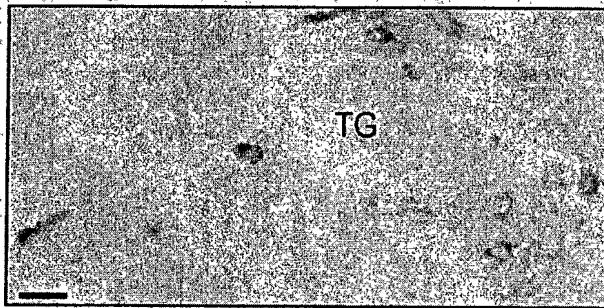


FIG. 9D

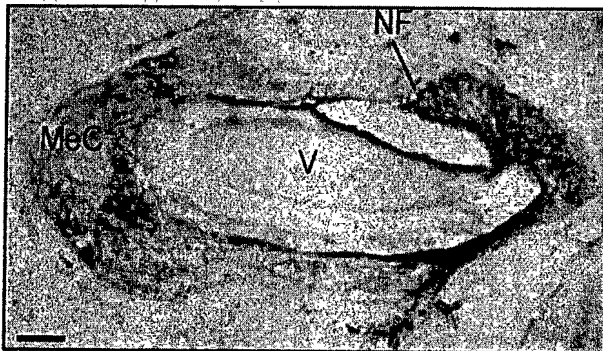


FIG. 9F

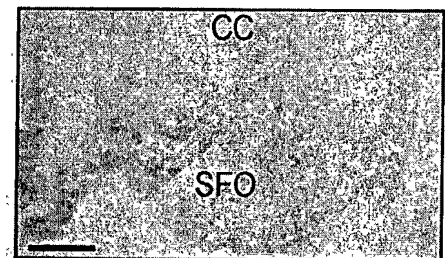


FIG. 9G

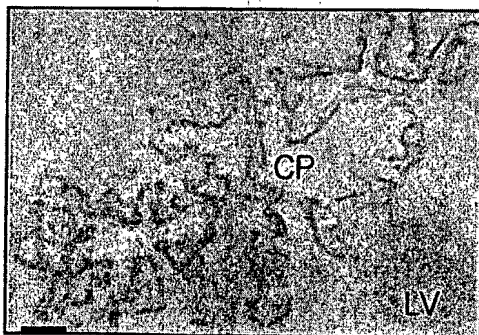
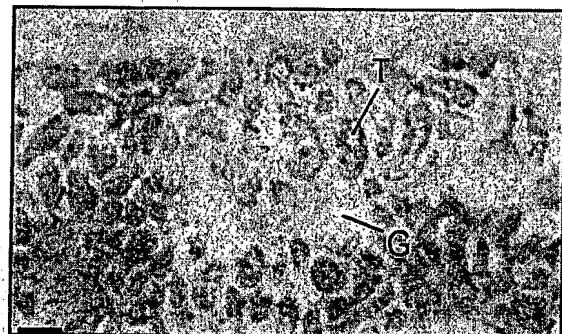


FIG. 9H



PATENT & TRADE-MARK OFFICE

FIG. 10A

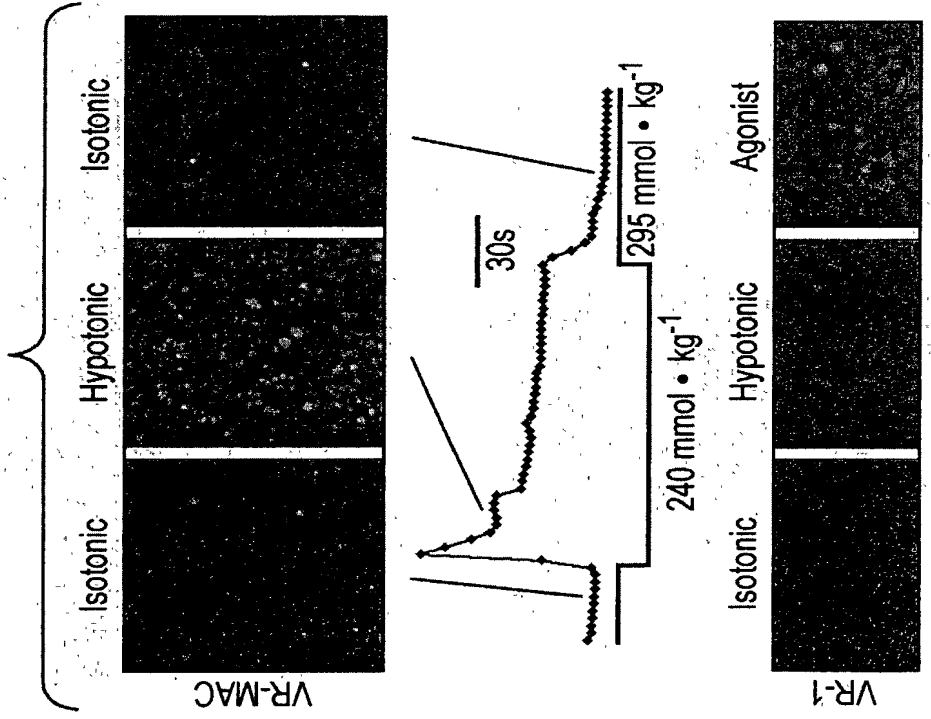


FIG. 10B

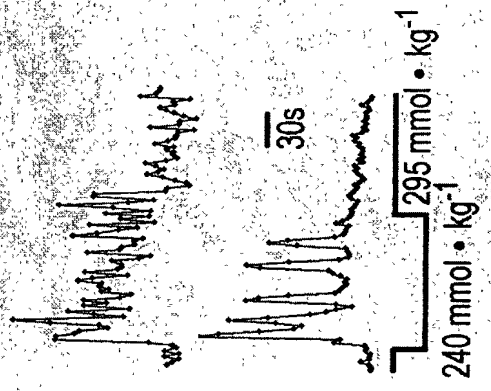
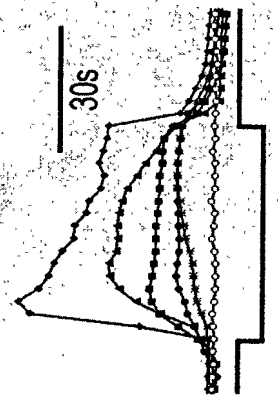


FIG. 10C





PATENT & TRADE-MARK OFF

FIG. 10D

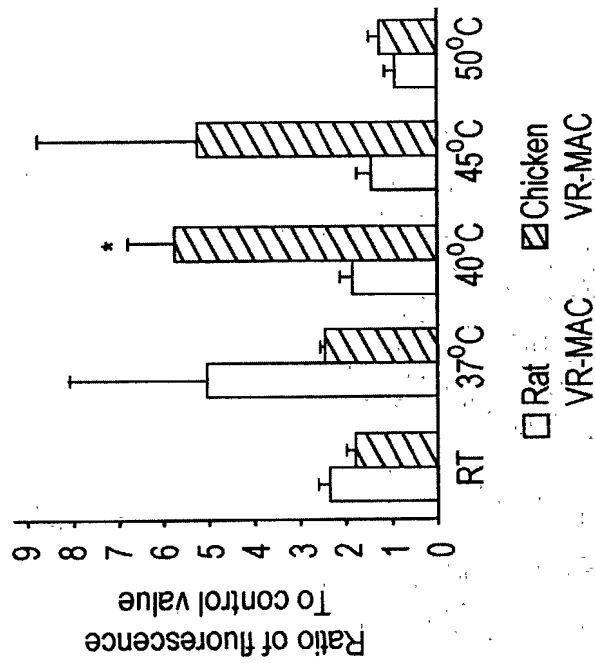


FIG. 10E

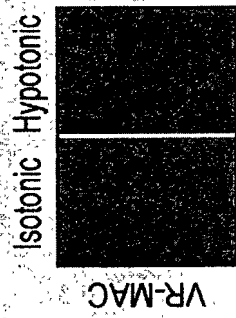


FIG. 10F

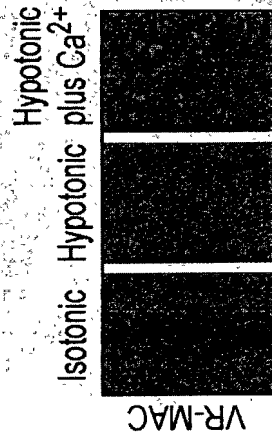




FIG. 11A

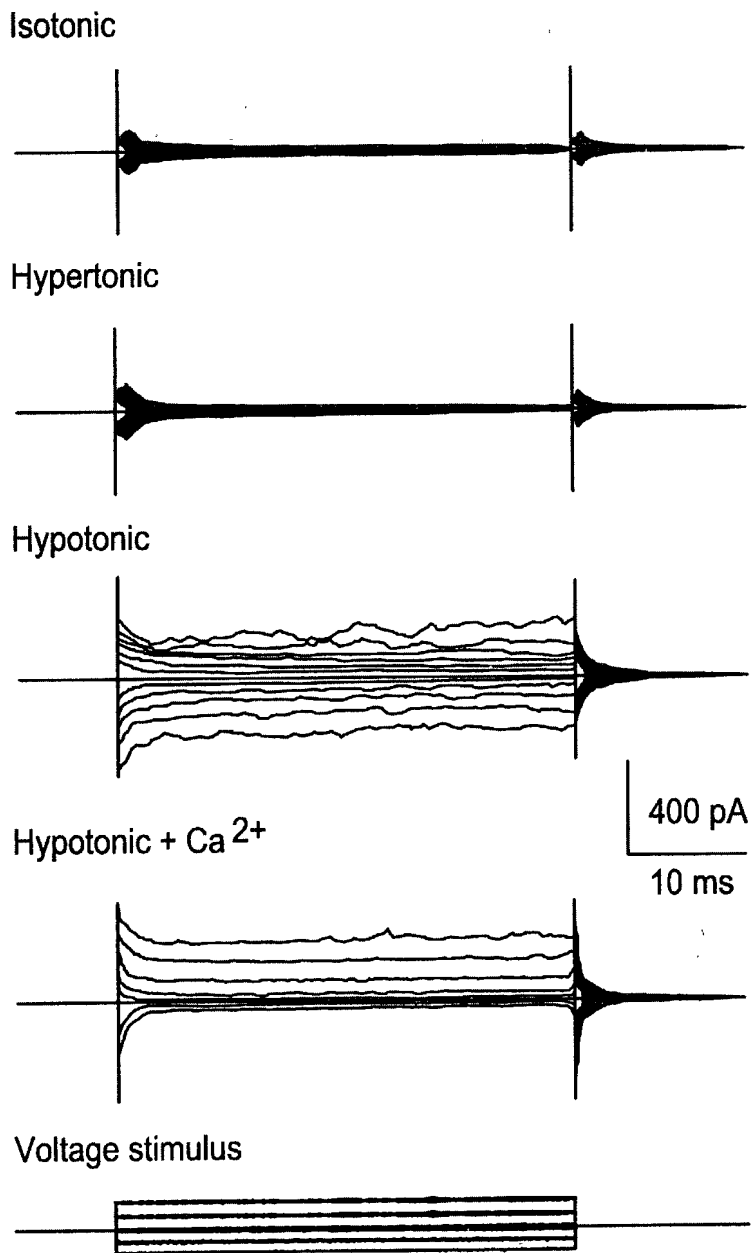




FIG. 11B

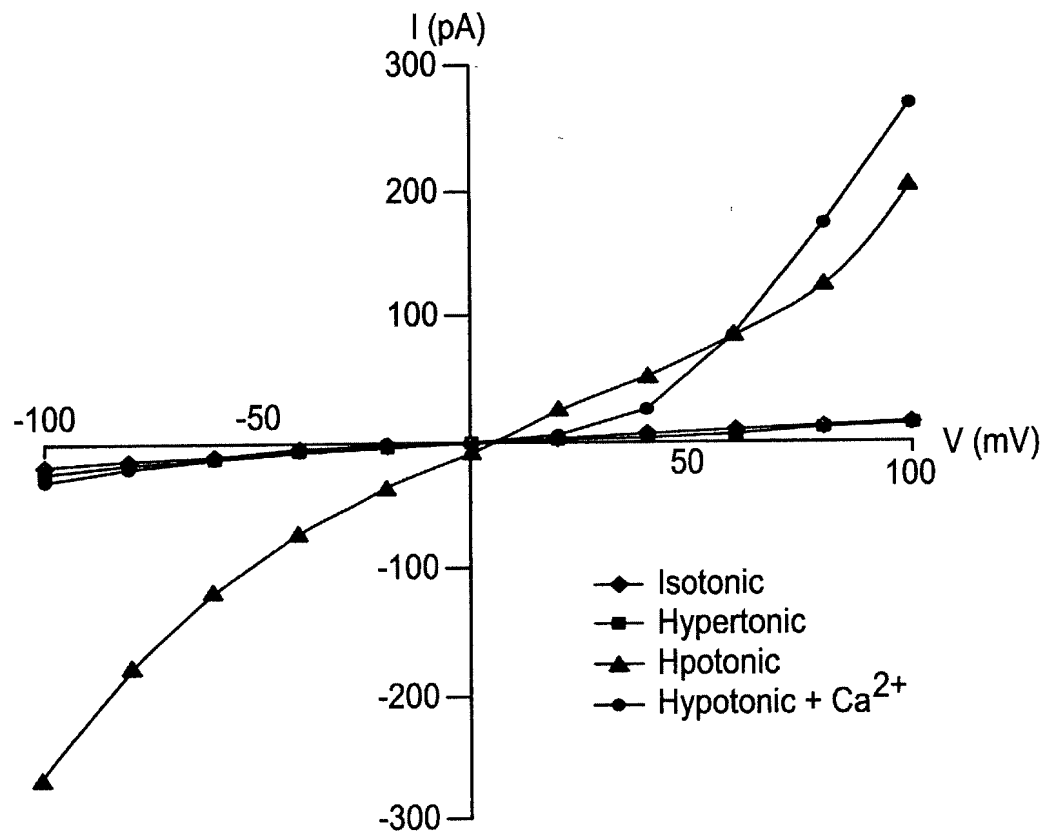
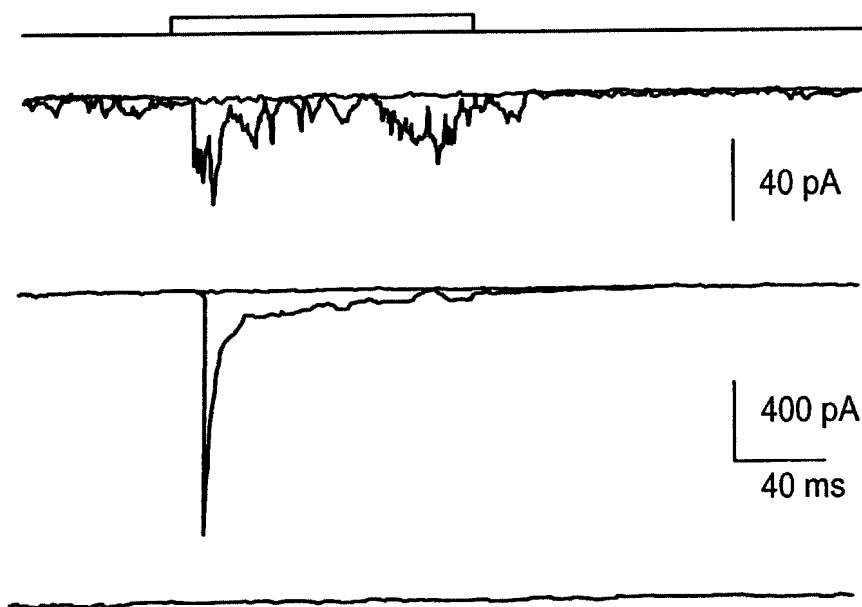


FIG. 11C



PATENT & TRADE MARK OFF

FIG. 12



PT & TRADEMARK OFFICE

FIG. 13A

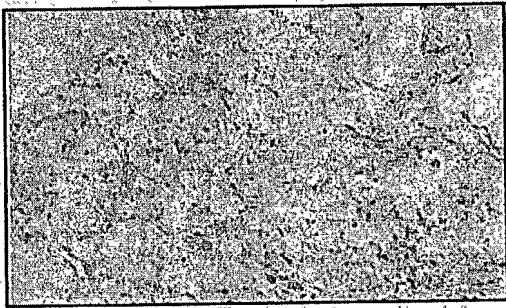


FIG. 13B

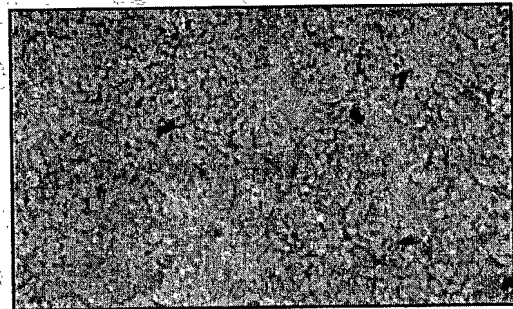


FIG. 13C



FIG. 13D



FIG. 13E

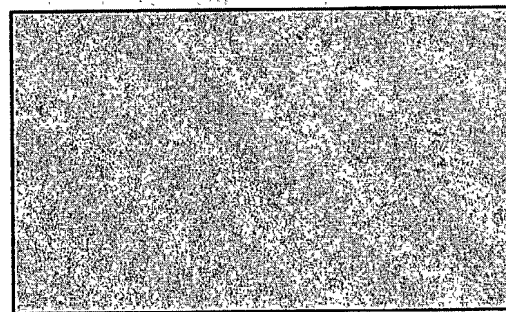
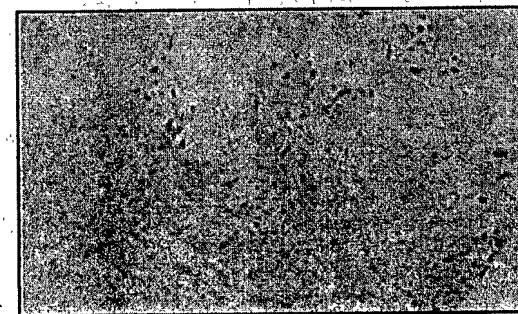


FIG. 13F



PATENT & TRADE MARK OFF

FIG. 13G

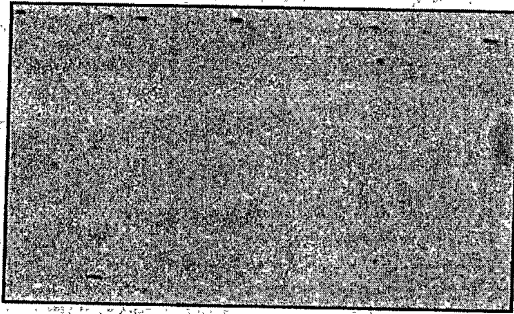


FIG. 13H

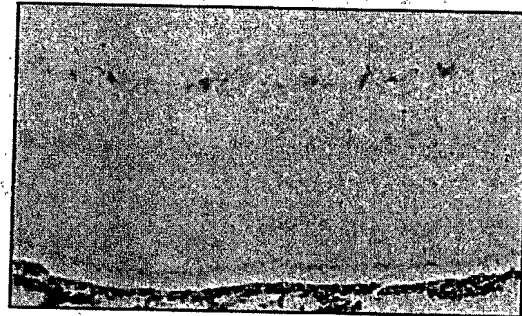


FIG. 13I

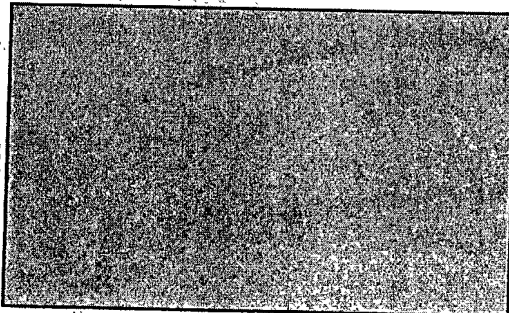
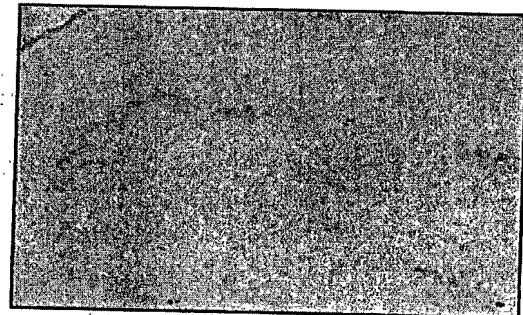


FIG. 13J



PATENT & TRADEMARK OFFICE

FIG. 14A-1

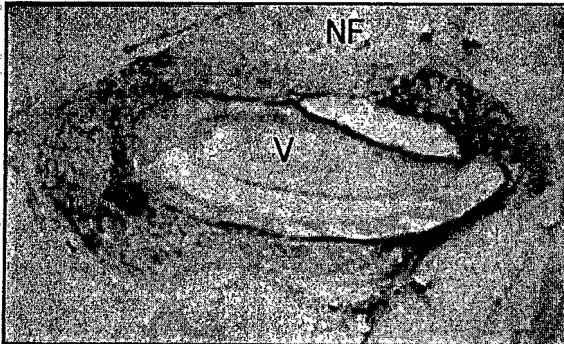


FIG. 14A-2

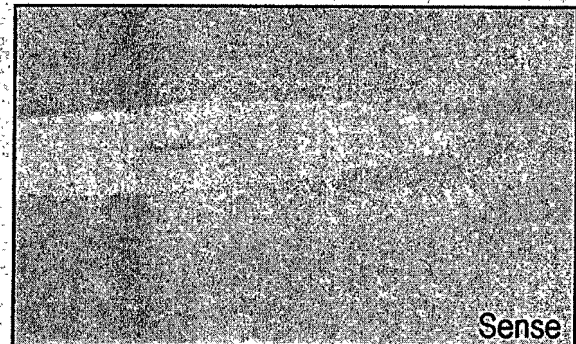


FIG. 14B-1

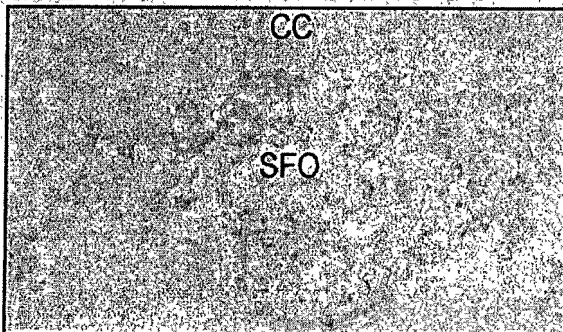


FIG. 14B-2

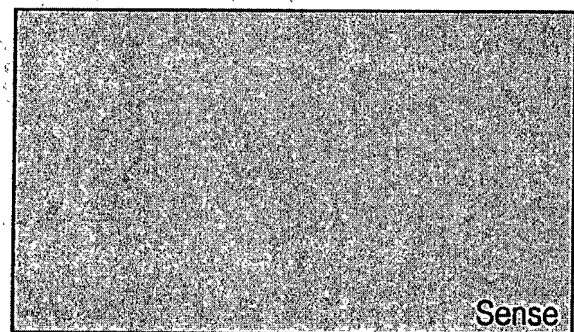


FIG. 14C-1

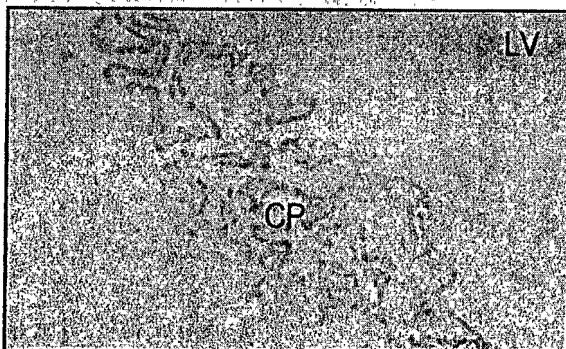
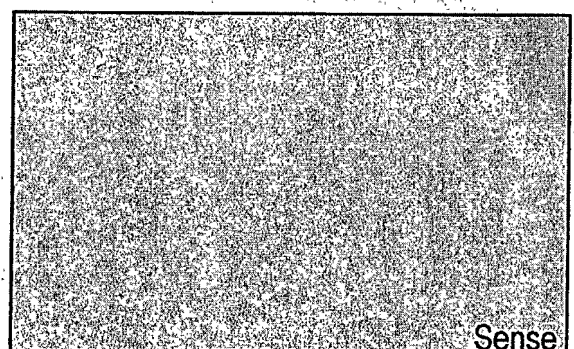


FIG. 14C-2





PATENT & TRADE-MARK

FIG. 14D-1

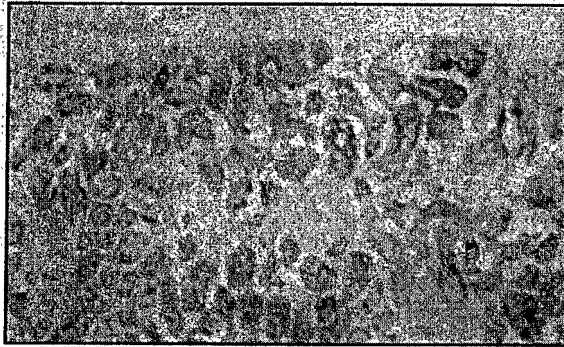


FIG. 14D-2

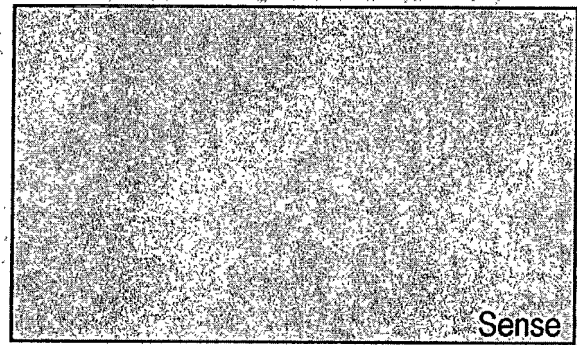


FIG. 14E

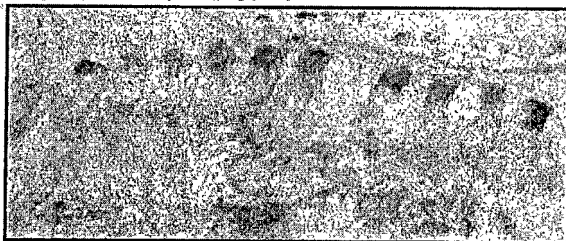
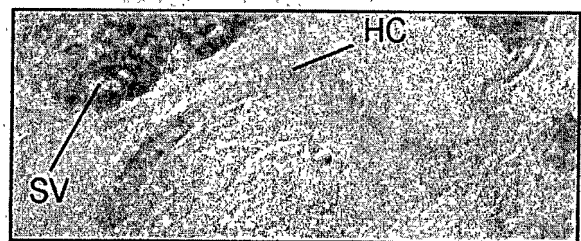


FIG. 14F







10027828, 002102

**FIG. 15A**  
Osmotic avoidance/  
basic paradigm

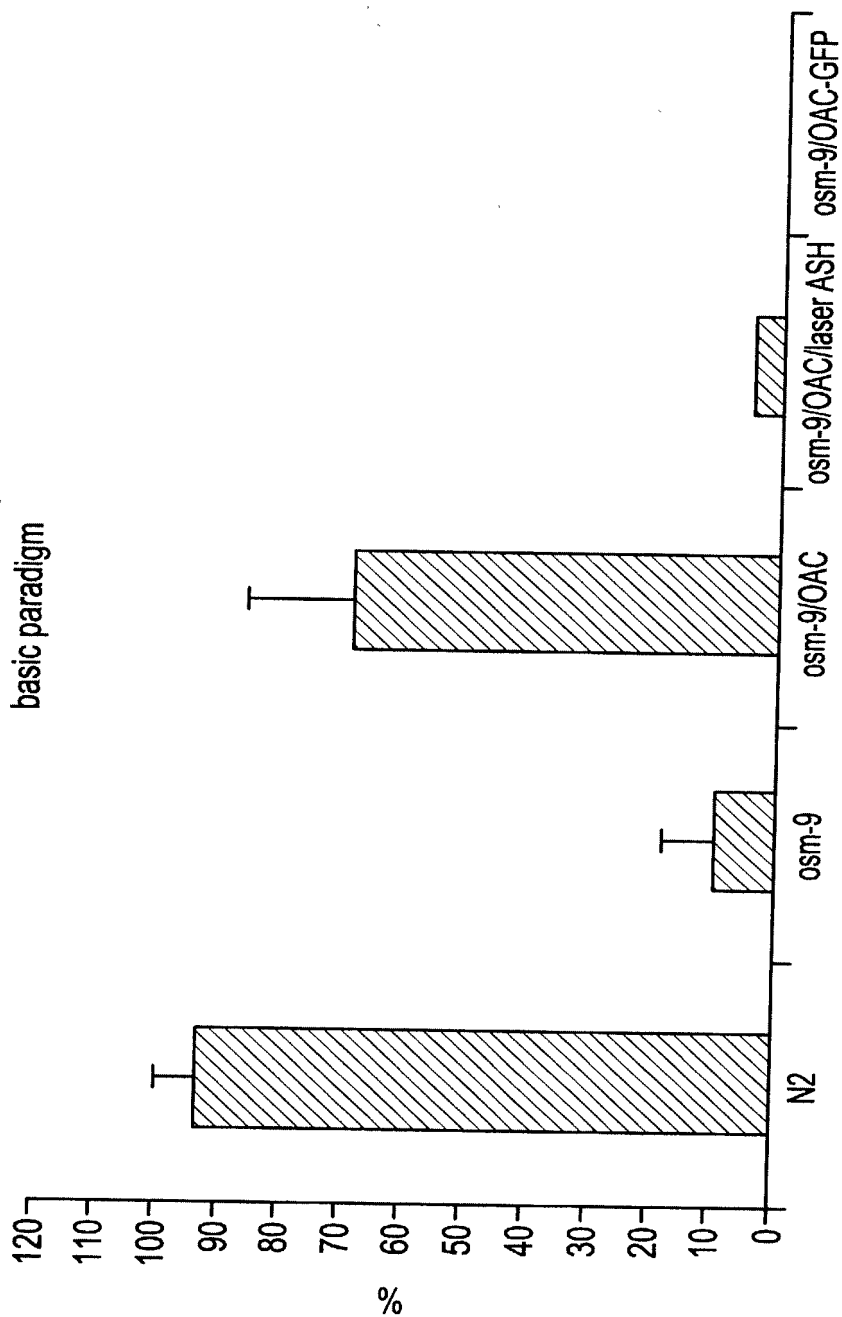




FIG. 15B

Nose touch  
basic paradigm

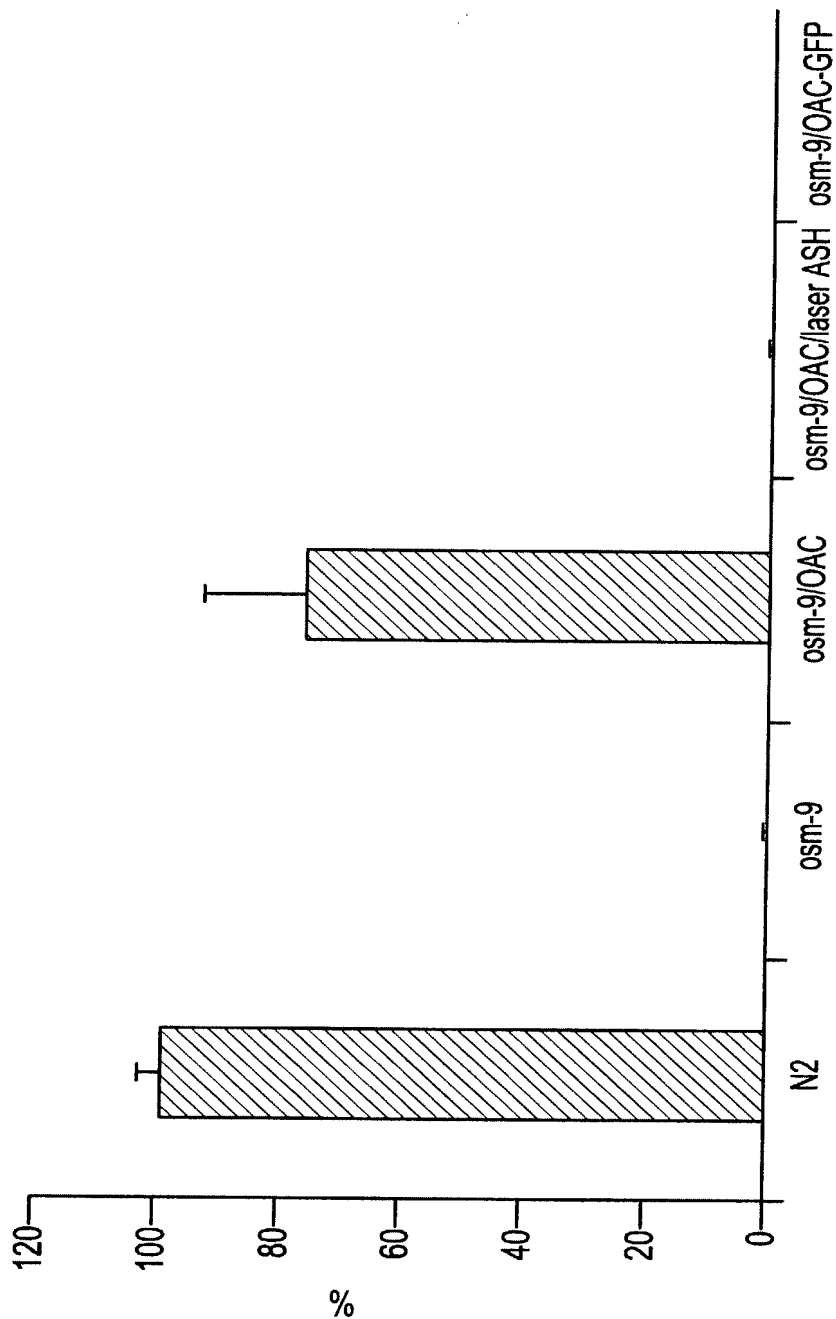
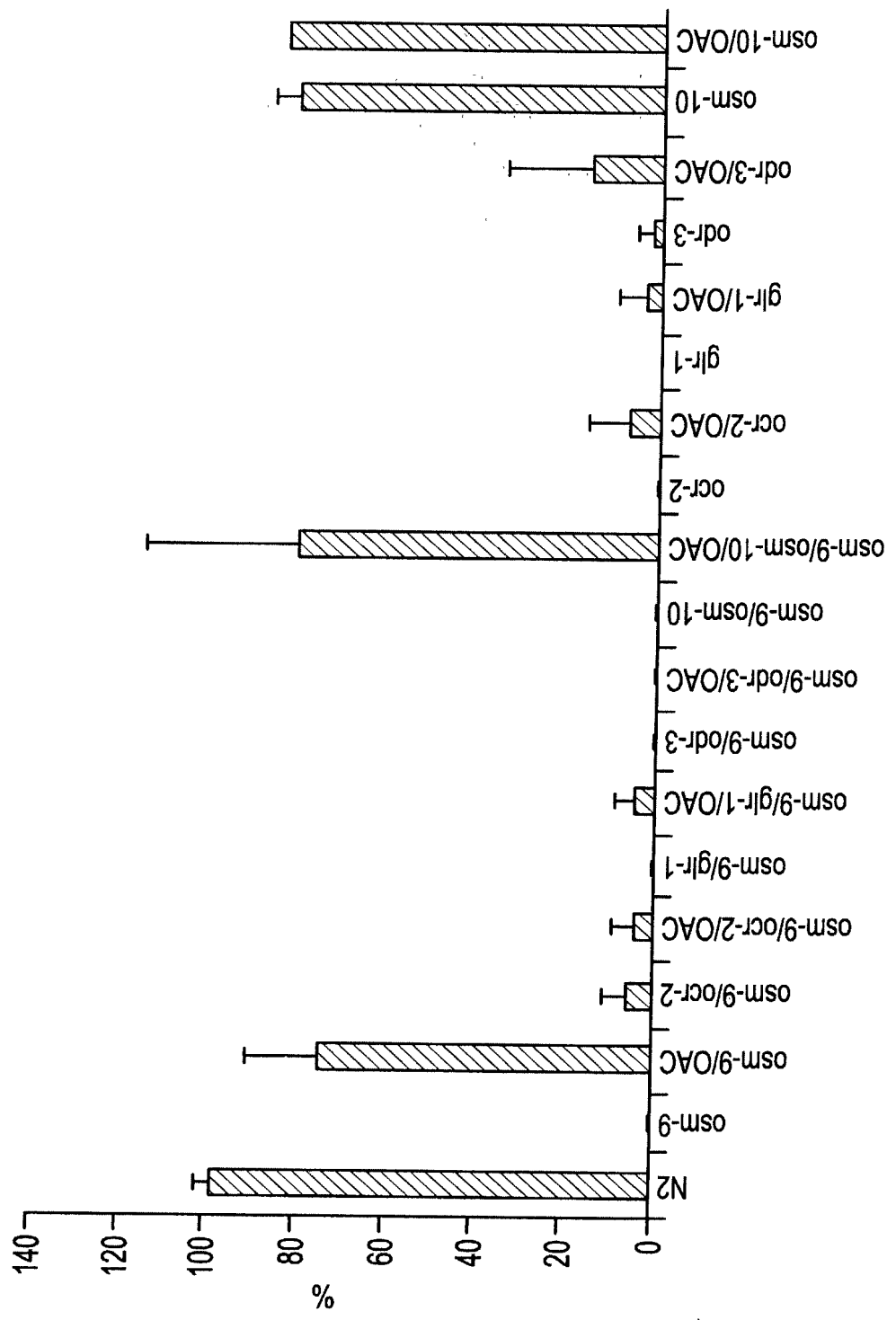




FIG. 16A

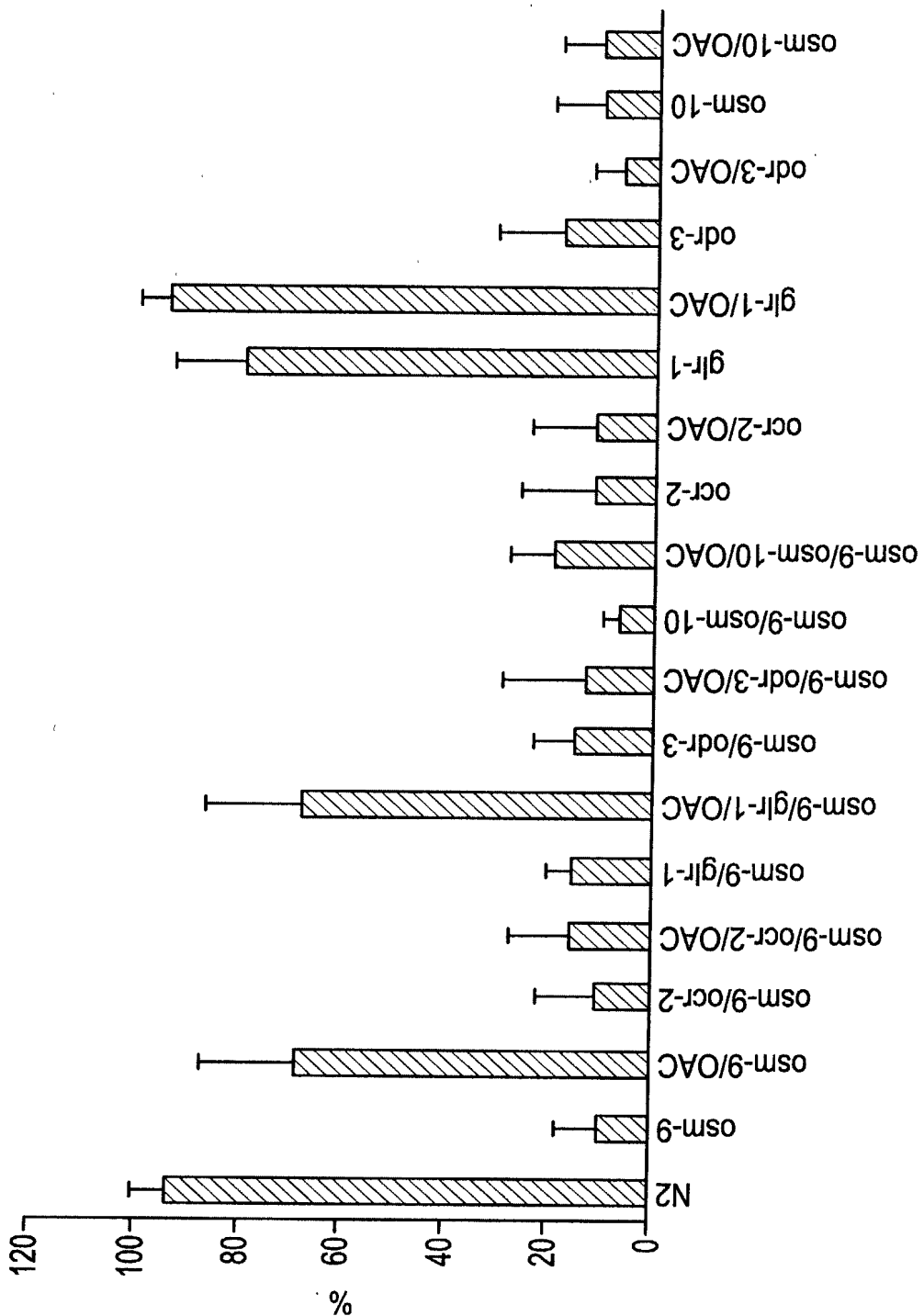
Nose touch  
alternate mechanosensory pathway





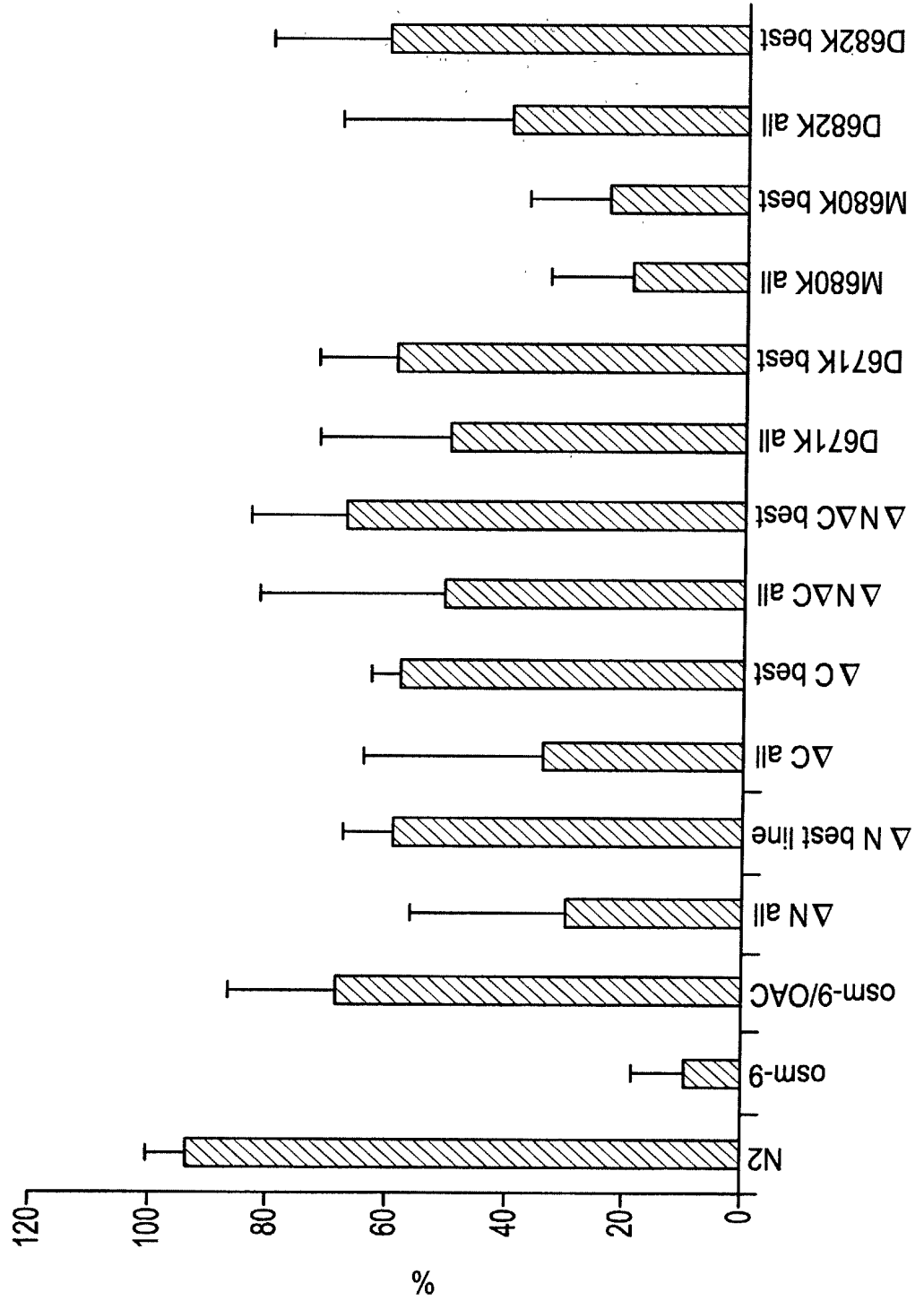
# FIG. 16B

Osmotic avoidance  
alternate mechanosensory pathway





**FIG. 17A**  
Osmotic avoidance  
structure-function study





**FIG. 17B**  
Nose touch  
structure-function study

